AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph on page 9, lines 8-11, with the following paragraph:

Figure 3. The aligned amino acid sequence of the LjNFR5 and PsSYM10 proteins. ~~Amino acid residues sharing identity are highlighted.~~ The *Medicago truncatula* (Ac126779) showing 76 % amino acid ~~identy~~identity to *Lotus* NFR5 is included to exemplify a substantial identical protein sequence.

Please replace the third paragraph on page 17, lines 20-24:

Pfam consensus: a consensus sequence derived from a large collection of protein multiple sequence alignments and profile hidden Markov models used to identify conserved protein domains (Bateman *et al.,* 2002, Nucleic Acids Res. 30: 276-80; and searchable on the internet at ~~http://www.~~ sanger.ac.uk/Software/Pfam[[/]] and on NCBI at ~~http://www.~~ ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi.

with the following paragraph:

Pfam consensus: a consensus sequence derived from a large collection of protein multiple sequence alignments and profile hidden Markov models used to identify conserved protein domains (Bateman *et al.,* 2002, Nucleic Acids Res. 30: 276-80; and searchable on the internet at sanger.ac.uk/Software/Pfam and on NCBI at ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi.

Please replace the fourth paragraph on page 17, lines 26-30:

Protein domain prediction: sequences are analyzed by BLAST ~~(www.~~ (ncbi.nlm.nih.gov/BLAST[[/]]) and PredictProtein ~~(www.~~ (emblheidelberg.de/predictprotein/predictprotein). Signal peptides are predicted by

SignalP v. 1.1 ~~(www.~~ (cbs.dtu.dk/services/signal[[/]]) and transmembrane regions are predicted by TMHMM v. 2.0 ~~(www.~~ (cbs.dtu.dk/services/TMHMM[[/]]).

with the following paragraph:

Protein domain prediction: sequences are analyzed by BLAST (ncbi.nlm.nih.gov/BLAST) and PredictProtein (emblheidelberg.de/predictprotein/predictprotein). Signal peptides are predicted by SignalP v. 1.1 (cbs.dtu.dk/services/signalP) and transmembrane regions are predicted by TMHMM v. 2.0 (cbs.dtu.dk/services/TMHMM).

Please replace the paragraph on page 19, lines 19-31 through page 20, lines 1-4:

Substantially identical: refers to two nucleic acid or polypeptide sequences that have at least about 60%, preferably about 65%, more preferably about 70%, further more preferably about 80%, most preferably about 90 or about 95% nucleotide or amino acid residue identity when aligned for maximum correspondence over a comparison window as measured using one of the sequence comparison algorithms given herein, or by manual alignment and visual inspection. This definition also refers to the complement of the test sequence with respect to its substantial identity to a reference sequence. A comparison window refers to any one of the number of contiguous positions in a sequence (being anything from between about 20 to about 600, most commonly about 100 to about 150) which may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Optimal alignment can be achieved using computerized implementations of alignment algorithms (e.g., GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, Wis. USA) or BLAST analyses available on the site: ~~(www~~ ncbi.nlm.nih.gov[[/)]].

with the following paragraph:

Substantially identical: refers to two nucleic acid or polypeptide sequences that have at least about 60%, preferably about 65%, more preferably about 70%, further more preferably about 80%, most preferably about 90 or about 95% nucleotide or amino acid residue identity when aligned for maximum correspondence over a comparison window as measured using one of the sequence comparison algorithms given herein, or by manual alignment and visual inspection. This definition also refers to the complement of the test sequence with respect to its substantial identity to a reference sequence. A comparison window refers to any one of the number of contiguous positions in a sequence (being anything from between about 20 to about 600, most commonly about 100 to about 150) which may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Optimal alignment can be achieved using computerized implementations of alignment algorithms (e.g., GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, Wis. USA) or BLAST analyses available on the site: ncbi.nlm.nih.gov.

Please replace the paragraph on page 53, lines 17-22, with the following:

Molecular markers based on DNA polymorphism are used to detect the alleles in breeding populations. Similar use can be taken of the *NFR1* sequences. Molecular DNA markers, based on the *NFR5* allele sequence differences of *Lotus* and pea, are bolded in Table 12 and highlighted in ~~Tables 12 and~~Table 13 as examples of how DNA polymorphism can be used directly to detect the presence of an advantageous allele in a breeding population.

Please replace Table 1 on page 55 with the following:

Table 1

Alignment of *Lotus*, *Glycine* and *Phaseolus* NFR5 protein sequences

	1	2	3	4	50
Lotus	MAVFF--	GSLSLFLALT	LLFTNIAARS	EKISGPDFSC	PVDSPPSCET
Glycine	MAVFFPFLPL	HSQILCLVIM	LFSTNIVAQS	QQDNRTNFSC	PSDSPPSCET
Phaseolus	MAVFFVSLTL	GAQILYVVLM	FFTC-	QQTNGTNFSC	PSNSPPSCET
	6	7	8	9	100
Lotus	YVTYTAQSPN	LLSLTNISD	FDISPLSIA	ASNIDAGKDK	LVPGQVLLVP
Glycine	YVTYIAQSPN	FLSLTNISN	FDTSPLSIAR	ASNLEPMDDK	LVKDQVLLVP
Phaseolus	YVTYISQSPN	FLSLTSVSN	FDTSPLSIAR	ASNLQHEEDK	LIPGQVLLI
	11	12	13	14	150
Lotus	VTCGCAGNHS	SANTSYQIQL	GDSYDFVATT	LYENLTNWNI	VQASNPGVNP
Glycine	VTCGCTGNRS	FANISYEINQ	GDSFYFVATT	SYENLTNWRA	VMDLNPVLSP
Phaseolus	VTCGCTGNRS	FANISYEINQ	GDSFYFVATT	LYQNLTNWHA	VMDLNPGLSQ
	16	17	18	19	200
Lotus	YLLPERVKVV	FPLFCRCPSK	NQLNKGIQYL	ITYVWKPNDN	VSLVSAKFGA
Glycine	NKLPIGIQVV	FPLFCKCPSK	NQLDKEIKYL	ITYVWKPGDN	VSLVSDKFGA
Phaseolus	FTLPIGIQV	IPLFCKCPSK	NQLDRGIKYL	ITHVWQPNDN	VSFVSNKLGA
	21	22	23	24	250
Lotus	SPADILTENR	YGQDFTAATN	LPILIPVTQ	PELTQPSSNG	RKSSIHLLV
Glycine	SPEDIMSENN	YGQNFTAANN	LPVLIPVTR	PVLARSPSDG	RKGGIRLPVI
Phaseolus	SPQDILSENN	YGQNFTAASN	LPVLIPVTL	PDLIQSPSDG	RKHRIGLPVI
	26	27	28	29	300
Lotus	LGITLGCTL	TAVLTGTLVY	VYCRRKKALN	RTASSAETAD	KLLSGVSGYV
Glycine	IGISLGCTL	VLVLAVLLVY	VYCLKMKTLN	RSASSAETAD	KLLSGVSGYV
Phaseolus	IGISLGCTL	VVVSAILLVC	VCCLKMKSLN	RSASSAETAD	KLLSGVSGYV
	31	32	33	34	350
Lotus	SKPNVYEIDE	IMEATKDFSD	ECKVGESVYK	ANIEGRVVAV	KKIKEGGANE
Glycine	SKPTMYETDA	IMEATMNLSE	QCKIGESVYK	ANIEGKVLAV	KRFKED-VTE
Phaseolus	SKPTMYETGA	ILEATMNLSE	QCKIGESVYK	ANIEGKVLAV	KRFKED-VTE
	36	37	38	39	400
Lotus	ELKILQKVNH	GNLVKLMGVS	SGYDGNCFLV	YEYAENGSLA	EWLFSKS--
Glycine	ELKILQKVNH	GNLVKLMGVS	SDNDGNCFVV	YEYAENGSLD	EWLFSKSCSD
Phaseolus	ELKILQKVNH	GNLVKLMGVS	SDNDGNCFVV	YEYAENGSLE	EWLFAKSCSE
	41	42	43	44	450
Lotus	-SGTPNSLTW	SQRISIAVDV	AVGLQYMHEH	TYPRIIHRD	TTSNILLDSN
Glycine	TSNSRASLTW	CQRISMAVDV	AMGLQYMHEH	AYPRIVHRDI	TSSNILLDSN
Phaseolus	TSNSRTSLTW	CQRISIAVDV	SMGLQYMHEH	AYPRIVHRDI	TSSNILLDSN
	46	47	48	49	500
Lotus	FKAKIANFAM	ARTSTNPMMP	KIDVFAFGVL	LIELLTGRKA	MTTKENGEVV
Glycine	FKAKIANFSM	ARTFTNPMMP	KIDVFAFGVV	LIELLTGRKA	MTTKENGEVV
Phaseolus	FKAKIANFSM	ARTFTNPMMS	KIDVFAFGVV	LIELLTGRKA	MTTKENGEVV

	51	52	53	54	550
Lotus	MLWKDMWEIF	DIEENREERI	RKWMDPNLES	FYHIDNALSL	ASLAVNCTAD
Glycine	MLWKDIWKIF	DQEENREERL	KKWMDPKLES	YYPIDYALSL	ASLAVNCTAD
Phaseolus	MLWKDIWKIF	DQEENREERL	RKWMDPKLDN	YYPIDYALSL	ASLAVNCTAD

	56	57	58	59	600
Lotus	KSLSRPSMAE	IVLSLSFLT	QSSNPTLERS	LTSSGLDVED	DAHIVTSIT
Glycine	KSLSRPTIAE	IVLSLSLLT	PSP-ATLERS	LTSSGLDVEA	-
Phaseolus	KSLSRPTIAE	IVLSLSLLT	PSP-ATLERS	LTSSGLDVEA	-

	61	62	63	65	650
Lotus	R....	....	....	....	.... SEQ ID NO: 8
Glycine	R....	....	....	....	.... SEQ ID NO: 48
Phaseolus	R....	....	....	....	.... SEQ ID NO: 40

Please replace Table 3 on page 57 with the following:

Table 3

Alignment of *Lotus* and *Pisum* NFR1 protein sequences

	1	2	3	4	50
Pisum	MKLKNGLLLF	F-	KVESKCVIGC	DIALASYYVM	P-
Pisum	MKLKNGLLLF	F-	KVDSKCVKGC	DLALASYYVM	P-
Lotus	MKLKTGLLLF	FILLLGHVC	HVESNCLKGC	DLALASYYI	PGVFILQNI

	6	7	8	9	100
Pisum	TFMQSKLVTN	SFEVIVRYNR	DIVFSNDNLF	SYFRVNIPFP	CECIGGEFLG
Pisum	NYMQSKIVTN	SSDVLNSYNK	VLVTNHGNIF	SYFRINIPF	CECIGGEFLG
Lotus	TFMQSEIVSS	N-	DKILNDINI	SFQRLNIPFP	CDCIGGEFLG

	11	12	13	14	150
Pisum	HVFEYTANEG	DTYDLIANTY	YASLTTVEVL	KKYNSYDPNH	IPVKAKVNVT
Pisum	HVFEYTTKKG	DTYDLIANNY	YVSLTSVELL	KKFNSYDPNH	IPAKAKVNVT
Lotus	HVFEYSASKG	DTYETIANL	YANLTTVDLL	KRFNSYDPKN	IPVNAKVNVT

	16	17	18	19	200
Pisum	VNCSCGNSQI	SKDYGLFITY	PLRPRDTLEK	IARHSNLDEG	VIQSYNLGVN
Pisum	VNCSCGNSQI	SKDYGLFVTY	PLRSTDSLEK	IANESKLDEG	LIQNFNPDVN
Lotus	VNCSCGNSQV	SKDYGLFITY	PIRPGDTLQD	IANQSSLDAG	LIQSFNPSVN

	21	22	23	24	250
Pisum	FSKGSGVVFF	PGRDKNGEYV	PLYPRT-GLG	KGAAAGISI	GIFALLLF
Pisum	FSRGSGIVF	PGRDKNGEYV	PLYPKT-GVG	KGVAIGISI	GVFAVLLFV
Lotus	FSKDSGIAF	PGRYKNGVYV	PLYHRTAGLA	SGAAVGISI	GTFVLLLLA

	26	27	28	29	300
Pisum	CIYIKYFQK	EEEKTKLP-Q	VSTALSAQD-	-ASGSGEYET	SGSSGHGTGS
Pisum	CIYVKYFQKK	EEEKTILP-	VSKALSTQDG	NASSSGEYET	SGSSGHGTGS
Lotus	CMYVRY-QKK	EEEKAKLPTD	ISMALSTQD	-ASSSAEYET	SGSSGPGTAS

	31	32	33	34	350
Pisum	TAGLTGIMVA	KSTEFSYQEL	AKATNNFSLD	NKIGQGGFGA	VYYAVLRGEK

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Pisum    AAGLTGIMVA  KSTEFSYQEL  AKATDNFSLD  NKIGQGGFGA  VYYAELRGEK
Lotus    ATGLTSIMVA  KSMEFSYQEL  AKATNNFSLD  NKIGQGGFGA  VYYAELRGKK

                 36          37          38          39         400
Pisum    TAIKKMDVQA  STEFLCELQV  LTHVHHLNLV  RLIGYCVEGS  LFLVYEHID
Pisum    TAIKKMNVQA  SSEFLCELKV  LTHVHHLNLV  RLIGYCVEGS  LFLVYEHID
Lotus    TAIKKMDVQA  STEFLCELKV  LTHVHHLNLV  RLIGYCVEGS  LFLVYEHID

                 41          42          43          44         450
Pisum    GNLGQYLHGI  DKAPLPWSSR  VQIALDSARG  LEYIHEHTVP  VYIHRDVKSA
Pisum    GNLGQYLHGK  DKEPLPWSSR  VQIALDSARG  LEYIHEHTVP  VYIHRDVKSA
Lotus    GNLGQYLHGS  GKEPLPWSSR  VQIALDAARG  LEYIHEHTVP  VYIHRDVKSA

                 46          47          48          49         500
Pisum    NILIDKNLH   KVADFGLTKL  IEVGNSTLHT  RLVGTFGYMP  PEYAQYGDVS
Pisum    NILIDKNLR   KVADFGLTKL  IEVGNSTLHT  RLVGTFGYMP  PEYAQYGDVS
Lotus    NILIDKNLR   KVADFGLTKL  IEVGNSTLQT  RLVGTFGYMP  PEYAQYGDIS

                 51          52          53          54         550
Pisum    PKIDVYAFGV  VLYELISAK   AILKTGESAV  -           EEALNQIDPL
Pisum    PKIDVYAFGV  VLYELISAK   AVLKTGEESV  AESKGLVALF  EKALNQIDPS
Lotus    PKIDVYAFGV  VLFELISAK   AVLKTGE-    AESKGLVALF  EEALNKSDPC

                 56          57          58          59         600
Pisum    EALRKLVDPR  LKENYPIDSV  LKMAQLGRAC  TRDNPLLRPS  MRSLVVALMT
Pisum    EALRKLVDPR  LKENYPIDSV  LKMAQLGRAC  TRDNPLLRPS  MRSLVVDLMT
Lotus    DALRKLVDPR  LGENYPIDSV  LKIAQLGRAC  TRDNPLLRPS  MRSLVVALMT

                 61          62          63          65         650
Pisum    LLSHTDD--   DTFYENQSLT  NLLSVR..    ....  SEQ ID NO: 52
Pisum    LSSPFEDCDD  DTSYENQTLI  NLLSVR..    ....  SEQ ID NO: 54
Lotus    LSSLTEDCDD  ESSYESQTLI  NLLSVR..    ....  SEQ ID NO: 24
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Please replace Table 12 on page 65 with the following:

Table 12

Nucleotide sequence variation between the pea *SYM10* alleles of pea cultivars Frisson and Finale*

Frisson	CTTGCATTTC	TTCACAATTT	CACAACAATG	GCTATCTTCT	TTCTTCCTTC
Finale	CTTGCATTTC	TTCACAATTT	CACAACAATG	GCTATCTTCT	TTCTTCCTTC
Frisson	TAGTTCTCAT	GCCCTTTTTC	TTGCACTCAT	GTTTTTTGTC	ACTAATATTT
Finale	TAGTTCTCAT	GCCCTTTTTC	TTGCACTCAT	GTTTTTTGTC	ACTAATATTT
Frisson	CAGCTCAACC	ATTACAACTC	AGTGGAACAA	ACTTTTCATG	CCCGGTGGAT
Finale	CAGCTCAACC	ATTACAACTC	AGTGGAACAA	ACTTTTCATG	CCCGGTGGAT
Frisson	TCACCTCCTT	CATGTGAAAC	CTATGTGACA	TACTTTGCTC	GGTCTCCAAA
Finale	TCACCTCCTT	CATGTGAAAC	CTATGTGACA	TACTTTGCTC	GGTCTCCAAA
Frisson	CTTTTTGAGC	CTAACTAACA	TATCAGATAT	ATTTGATATG	AGTCCTTTAT
Finale	CTTTTTGAGC	CTAACTAACA	TATCAGATAT	ATTTGATATG	AGTCCTTTAT
Frisson	CCATTGCAAA	AGCCAGTAAC	ATAGAAGATG	AGGACAAGAA	GCTGGTTGAA
Finale	CCATTGCAAA	AGCCAGTAAC	ATAGAAGATG	AGGACAAGAA	GCTGGTTGAA
Frisson	GGCCAAGTCT	TACTCATACC	TGTAACTTGT	GGTTGCACTA	GAAATCGCTA
Finale	GGCCAAGTCT	TACTCATACC	TGTAACTTGT	GGTTGCACTA	GAAATCGCTA
Frisson	TTTCGCGAAT	TTCACGTACA	CAATCAAGCT	AGGTGACAAC	TATTTCATAG
Finale	TTTCGCGAAT	TTCACGTACA	CAATCAAGCT	AGGTGACAAC	TATTTCATAG
Frisson	TTTCAACCAC	TTCATACCAG	AATCTTACAA	ATTATGTGGA	AATGGAAAAT
Finale	TTTCAACCAC	TTCATACCAG	AATCTTACAA	ATTATGTGGA	AATGGAAAAT
Frisson	TTCAACCCTA	ATCTAAGTCC	AAATCTATTG	CCACCAGAAA	TCAAAGTTGT
Finale	TTCAACCCTA	ATCTAAGTCC	AAATCTATTG	CCACCAGAAA	TCAAAGTTGT
Frisson	TGTCCCTTTA	TTCTGCAAAT	GCCCCTCGAA	GAATCAGTTG	AGCAAAGGAA
Finale	TGTCCCTTTA	TTCTGCAAAT	GCCCCTCGAA	GAATCAGTTG	AGCAAAGGAA
Frisson	TAAAGCATCT	GATTACTTAT	GTGTGGCAGG	CTAATGACAA	TGTTACCCGT
Finale	TAAAGCATCT	GATTACTTAT	GTGTGGCAGG	CTAATGACAA	TGTTACCCGT
Frisson	GTAAGTTCCA	AGTTTGGTGC	ATCACAAGTG	GATATGTTTA	CTGAAAACAA
Finale	GTAAGTTCCA	AGTTTGGTGC	ATCACAAGTG	GATATGTTTA	CTGAAAACAA
Frisson	TCAAAACTTC	ACTGCTTCAA	CCAA**C**GTTCC	GATTTTGATC	CCTGTGACAA
Finale	TCAAAACTTC	ACTGCTTCAA	CCAA**T**GTTCC	GATTTTGATC	CCTGTGACAA

Frisson	AGTTACCGGT AATTGATCAA CCATCTTCAA ATGGAAGAAA AAACAGCACT
Finale	AGTTACCGGT AATTGATCAA CCATCTTCAA ATGGAAGAAA AAACAGCACT
Frisson	CAAAAACCTG CTTTTATAAT TGGTATTAGC CTAGGATGTG CTTTTTTCGT
Finale	CAAAAACCTG CTTTTATAAT TGGTATTAGC CTAGGATGTG CTTTTTTCGT
Frisson	TGTAGTTTTA ACACTATCAC TTGTTTATGT ATATTGTCTG AAAATGAAGA
Finale	TGTAGTTTTA ACACTATCAC TTGTTTATGT ATATTGTCTG AAAATGAAGA
Frisson	GATTGAATAG GAGTACTTCA TTGGCGGAGA CTGCGGATAA GTTACTTTCA
Finale	GATTGAATAG GAGTACTTCA TTGGCGGAGA CTGCGGATAA GTTACTTTCA
Frisson	GGTGTTTCGG GTTATGTAAG CAAGCCAACA ATGTATGAAA TGGATGCGAT
Finale	GGTGTTTCGG GTTATGTAAG CAAGCCAACA ATGTATGAAA TGGATGCGAT
Frisson	CATGGAAGCT ACAATGAACC TGAGTGAGAA TTGTAAGATT GGTGAATC**C**G
Finale	CATGGAAGCT ACAATGAACC TGAGTGAGAA TTGTAAGATT GGTGAATC**T**G
Frisson	TTTACAAGGC TAATATAGAT GGTAGAGTTT TAGCAGTGAA AAAAATCAAG
Finale	TTTACAAGGC TAATATAGAT GGTAGAGTTT TAGCAGTGAA AAAAATCAAG
Frisson	AAAGATGCTT CTGAGGAGCT GAAAATT**T**TG CAGAAGGTAA ATCATGGAAA
Finale	AAAGATGCTT CTGAGGAGCT GAAAATT**C**TG CAGAAGGTAA ATCATGGAAA
Frisson	TCTTGTGAAA CTTATGGGTG TGTCTTCCGA CAACGA**C**GGA AACTGTTTCC
Finale	TCTTGTGAAA CTTATGGGTG TGTCTTCCGA CAACGA**A**GGA AACTGTTTCC
Frisson	TTGTTTACGA GTATGCTGAA AATGGATCAC TTGATGAGTG GTTGTTCTCA
Finale	TTGTTTACGA GTATGCTGAA AATGGATCAC TTGATGAGTG GTTGTTCTCA
Frisson	GAGT**C**GTCGA AAACTTCGAA CTCGGTGGTC TCGCTTACAT GGTCTCAGAG
Finale	GAGT**T**GTCGA AAACTTCGAA CTCGGTGGTC TCGCTTACAT GGTCTCAGAG
Frisson	AATAACAGTA GCAGTGGATG TTGCAGTTGG TTTGCAATAC ATGCATGAAC
Finale	AATAACAGTA GCAGTGGATG TTGCAGTTGG TTTGCAATAC ATGCATGAAC
Frisson	ATACTTACCC AAGAATAATC CACAGAGACA TCACAACAAG TAATATCCTT
Finale	ATACTTACCC AAGAATAATC CACAGAGACA TCACAACAAG TAATATCCTT
Frisson	CTGGATTCAA ACTTTAAGGC CAAGATAGCG AATTTTTCAA TGGCCAGAAC
Finale	CTGGATTCAA ACTTTAAGGC CAAGATAGCG AATTTTTCAA TGGCCAGAAC
Frisson	TTCAACAAAT TCCATGATGC CGAAAATCGA TGTTTTCGCT TTTGGGGTGG
Finale	TTCAACAAAT TCCATGATGC CGAAAATCGA TGTTTTCGCT TTTGGGGTGG
Frisson	TTCTGATTGA GTTGCTTACC GGCAAGAAAG CGATAACAAC GATGGAAAAT
Finale	TTCTGATTGA GTTGCTTACC GGCAAGAAAG CGATAACAAC GATGGAAAAT
Frisson	GGCGAGGTGG TTATTCTGTG GAAGGATTTC TGGAAGATTT TTGATCTAGA
Finale	GGCGAGGTGG TTATTCTGTG GAAGGATTTC TGGAAGATTT TTGATCTAGA

Frisson	AGGGAATAGA	GAAGAGAGCT	TAAGAAAATG	GATGGATCCT	AAGCTAGAGA
Finale	AGGGAATAGA	GAAGAGAGCT	TAAGAAAATG	GATGGATCCT	AAGCTAGAGA
Frisson	ATTTTTATCC	TATTGATAAT	GCTCTTAGTT	TGGCTTCTTT	GGCAGTGAAT
Finale	ATTTTTATCC	TATTGATAAT	GCTCTTAGTT	TGGCTTCTTT	GGCAGTGAAT
Frisson	TGTACTGCAG	ATAAATCATT	GTCAAGACCA	AGCATTGCAG	AAATTGTTCT
Finale	TGTACTGCAG	ATAAATCATT	GTCAAGACCA	AGCATTGCAG	AAATTGTTCT
Frisson	TTGTCTTTCT	CTTCTCAATC	AATCATCATC	TGAACCAATG	TTAGAAAGAT
Finale	TTGTCTTTCT	CTTCTCAATC	AATCATCATC	TGAACCAATG	TTAGAAAGAT
Frisson	CCTTGACATC	TGGTTTAGAT	GTTGAAGCTA	CTCATGTTGT	TACTTCTATA
Finale	CCTTGACATC	TGGTTTAGAT	GTTGAAGCTA	CTCATGTTGT	TACTTCTATA
Frisson	GTAGCTCGTT	GATATTCATT	CAAGTGAAGG	TAACACT**G**AA	TCAATGCTTC
Finale	GTAGCTCGTT	GATATTCATT	CAAGTGAAGG	TAACACT**A**AA	TCAATGCTTC
Frisson	AGTTTCTTAT	ATTCAAGATG	GTTACTTTGT	TTAG**A**TGATT	ATTGATTACA
Finale	AGTTTCTTAT	ATTCAAGATG	GTTACTTTGT	TTAG**G**TGATT	ATTGATTACA
Frisson	TCTTTATGTG	TGGAACTATA	TGGTTATTTT	AATTAAGGGA	ATT**G**TTCTAA
Finale	TCTTTATGTG	TGGAACTATA	TGGTTATTTT	AATTAAGGGA	ATT**A**GTCTAA
Frisson	A**A**TTCATTTT	TCCATGTT	SEQ ID NO: 13		
Finale	A**T**TTCATTTT	TCCATGTT	SEQ ID NO: 12		

* Nucleotide differences are bolded and the coding region is underlined